

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ruben, Steven M
- (ii) TITLE OF INVENTION: Apoptosis Inducing Molecule I
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Human Genome Sciences, Inc.
  - (B) STREET: 9410 Key West Avenue
  - (C) CITY: Rockville
  - (D) STATE: MD
  - (E) COUNTRY: US
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 13-MAR-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Kimball, Paul, C.
  - (B) REGISTRATION NUMBER: 34,610
  - (C) REFERENCE/DOCKET NUMBER: PF261
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (301) 309-8504
  - (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 52..894
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGCG GCTGCCTGGC TGAATTACAG CAGTCAGACT CTGACAGGTT C ATG GCT  
Met Ala  
1

57

ATG ATG GAG GTC CAG GGG GGA CCC AGC CTG GGA CAG ACC TGC GTG CTG	105
Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys Val Leu	
5 10 15	
ATC GTG ATC TTC ACA GTG CTC CTG CAG TCT CTC TGT GTG GCT GTA ACT	153
Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala Val Thr	
20 25 30	
TAC GTG TAC TTT ACC AAC GAG CTG AAG CAG ATG CAG GAC AAG TAC TCC	201
Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser	
35 40 45 50	
AAA AGT GGC ATT GCT TGT TTC TTA AAA GAA GAT GAC AGT TAT TGG GAC	249
Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp	
55 60 65	
CCC AAT GAC GAA GAG AGT ATG AAC AGC CCC TGC TGG CAA GTC AAG TGG	297
Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val Lys Trp	
70 75 80	
CAA CTC CGT CAG CTC GTT AGA AAG ATG ATT TTG AGA ACC TCT GAG GAA	345
Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu	
85 90 95	
ACC ATT TCT ACA GTT CAA GAA AAG CAA CAA AAT ATT TCT CCC CTA GTG	393
Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val	
100 105 110	
AGA GAA AGA GGT CCT CAG AGA GTA GCA GCT CAC ATA ACT GGG ACC AGA	441
Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg	
115 120 125 130	
GGA AGA AGC AAC ACA TTG TCT TCT CCA AAC TCC AAG AAT GAA AAG GCT	489
Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala	
135 140 145	
CTG GGC CGC AAA ATA AAC TCC TGG GAA TCA TCA AGG AGT GGG CAT TCA	537
Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser	
150 155 160	
TTC CTG AGC AAC TTG CAC TTG AGG AAT GGT GAA CTG GTC ATC CAT GAA	585
Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu	
165 170 175	
AAA GGG TTT TAC TAC ATC TAT TCC CAA ACA TAC TTT CGA TTT CAG GAG	633
Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu	
180 185 190	
GAA ATA AAA GAA AAC ACA AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT	681
Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile	
195 200 205 210	
TAC AAA TAC ACA AGT TAT CCT GAC CCT ATA TTG TTG ATG AAA AGT GCT	729
Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala	
215 220 225	
AGA AAT AGT TGT TGG TCT AAA GAT GCA GAA TAT GGA CTC TAT TCC ATC	777
Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile	
230 235 240	

TAT CAA GGG GGA ATA TTT GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT	825
Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val	
245 250 255	
TCT GTA ACA AAT GAG CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT	873
Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe	
260 265 270	
TTC GGG GCC TTT TTA GTT GGC TAACTGACCT GGAAAGAAAA AGCAATAACC	924
Phe Gly Ala Phe Leu Val Gly	
275 280	
TCAAAGTGAC TATTCAGTTT TCAGGATGAT ACACTATGAA GATGTTTCAA AAAATCTGAC	984
CAAAACAAAC AAACAGAAAA CAGAAAACAA AAAAACCTCT ATGCAATCTG AGTAGAGCAG	1044
CCACAACCAA AAAATTCTAC AACACACACT GTTCTGAAAG TGA CTCACTT ATCCCAAGAA	1104
AATGAAATTG CTGAAAGATC TTTCAGGACT CTACCTCATA TCAGTTTGCT AGCAGAAATC	1164
TAGAAGACTG TCAGCTTCCA AACATTAATG CAATGGTTAA CATCTTCTGT CTTTATAATC	1224
TACTCCTTGT AAAGACTGTA GAAGAAAGCG CAACAATCCA TCTCTCAAGT AGTGTATCAC	1284
AGTAGTAGCC TCCAGGTTTC CTTAAGGGAC AACATCCTTA AGTCAAAAGA GAGAAGAGGC	1344
ACCACTAAAA GATCGCAGTT TGCCTGGTGC AGTGGCTCAC ACCTGTAATC CCAACATTTT	1404
GGGAACCCAA GGTGGGTAGA TCACGAGATC AAGAGATCAA GACCATAGTG ACCAACATAG	1464
TGAAACCCCA TCTCTACTGA AAGTGCAAAA ATTAGCTGGG TGTGTTGGCA CATGCCTGTA	1524
GTCCCAGCTA CTTGAGAGGC TGAGGCAGGA GAATCGTTTG AACCCGGGAG GCAGAGGTTG	1584
CAGTGTGGTG AGATCATGCC ACTACACTCC AGCCTGGCGA CAGAGCGAGA CTTGGTTTC	1643

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys	
1 5 10 15	
Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala	
20 25 30	
Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys	
35 40 45	
Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr	
50 55 60	

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val  
 65 70 75 80  
 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser  
 85 90 95  
 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro  
 100 105 110  
 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly  
 115 120 125  
 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu  
 130 135 140  
 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly  
 145 150 155 160  
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile  
 165 170 175  
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe  
 180 185 190  
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln  
 195 200 205  
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys  
 210 215 220  
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr  
 225 230 235 240  
 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile  
 245 250 255  
 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala  
 260 265 270  
 Ser Phe Phe Gly Ala Phe Leu Val Gly  
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 267 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu  
 1 5 10 15

Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro  
                     20                    25                    30  
 Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro  
                     35                    40                    45  
 Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser  
                     50                    55                    60  
 Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu  
                     65                    70                    75                    80  
 Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu  
                     85                    90                    95  
 Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser  
                     100                    105                    110  
 Leu Glu Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu  
                     115                    120                    125  
 Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met  
                     130                    135                    140  
 Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val  
                     145                    150                    155                    160  
 Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe  
                     165                    170                    175  
 Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro  
                     180                    185                    190  
 Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu  
                     195                    200                    205  
 Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met  
                     210                    215                    220  
 Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala  
                     225                    230                    235                    240  
 Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu  
                     245                    250                    255  
 Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu  
                     260                    265

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gln	Gln	Pro	Met	Asn	Tyr	Pro	Cys	Pro	Gln	Ile	Phe	Trp	Val	Asp	
1				5				10						15		
Ser	Ser	Ala	Thr	Ser	Ser	Trp	Ala	Pro	Pro	Gly	Ser	Val	Phe	Pro	Cys	
			20					25					30			
Pro	Ser	Cys	Gly	Pro	Arg	Gly	Pro	Asp	Gln	Arg	Arg	Pro	Pro	Pro	Pro	
		35					40					45				
Pro	Pro	Pro	Val	Ser	Pro	Leu	Pro	Pro	Pro	Ser	Gln	Pro	Leu	Pro	Leu	
	50					55					60					
Pro	Pro	Leu	Thr	Pro	Leu	Lys	Lys	Lys	Asp	His	Asn	Thr	Asn	Leu	Trp	
65					70				75					80		
Leu	Pro	Val	Val	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly	Met	Gly	
				85					90					95		
Leu	Gly	Met	Tyr	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Leu	Ala	Glu	Leu	
			100					105					110			
Arg	Glu	Phe	Thr	Asn	Gln	Ser	Leu	Lys	Val	Ser	Ser	Phe	Glu	Lys	Gln	
		115					120					125				
Ile	Ala	Asn	Pro	Ser	Thr	Pro	Ser	Glu	Lys	Lys	Glu	Pro	Arg	Ser	Val	
	130					135					140					
Ala	His	Leu	Thr	Gly	Asn	Pro	His	Ser	Arg	Ser	Ile	Pro	Leu	Glu	Trp	
145					150				155					160		
Glu	Asp	Thr	Tyr	Gly	Thr	Ala	Leu	Ile	Ser	Gly	Val	Lys	Tyr	Lys	Lys	
				165					170				175			
Gly	Gly	Leu	Val	Ile	His	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr	Ser	Lys	
			180					185					190			
Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Gln	Pro	Leu	Asn	His	Lys	
		195					200					205				
Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Glu	Asp	Leu	Val	Leu	Met	Glu	
	210					215					220					
Glu	Lys	Arg	Leu	Asn	Tyr	Cys	Thr	Thr	Gly	Gln	Ile	Trp	Ala	His	Ser	
225				230					235					240		
Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His	Leu	Tyr	
				245					250				255			
Val	Asn	Ile	Ser	Gln	Leu	Ser	Leu	Ile	Asn	Phe	Glu	Glu	Ser	Lys	Thr	
			260					265					270			
Phe	Phe	Gly	Leu	Tyr	Lys	Leu										
			275													

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1           5           10           15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
          20           25           30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
          35           40           45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
          50           55           60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65           70           75           80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
          85           90           95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
          100          105          110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
          115          120          125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
          130          135          140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145           150           155           160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
          165          170          175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
          180          185          190

Pro Ile Tyr Leu Gly Cys Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
          195          200          205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
          210          215          220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225           230

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(2) INFORMATION FOR SEQ ID NO:6:

(ii) MOLECULE TYPE: protein

Met 1	Thr	Pro	Pro	Glu 5	Arg	Leu	Phe	Leu	Pro 10	Arg	Val	Cys	Gly	Thr 15	Thr
Leu	His	Leu	Leu 20	Leu	Leu	Gly	Leu	Leu 25	Leu	Val	Leu	Leu	Pro 30	Gly	Ala
Gln	Gly	Leu 35	Pro	Gly	Val	Gly 40	Leu	Thr	Pro	Ser	Ala 45	Ala	Gln	Thr	Ala
Arg 50	Gln	His	Pro	Lys	Met	His 55	Leu	Ala	His	Ser	Thr 60	Leu	Lys	Pro	Ala
Ala 65	His	Leu	Ile	Gly	Asp 70	Pro	Ser	Lys	Gln	Asn 75	Ser	Leu	Leu	Trp	Arg 80
Ala	Asn	Thr	Asp 85	Arg	Ala	Phe	Leu	Gln 90	Asp	Gly	Phe	Ser	Leu	Ser 95	Asn
Asn	Ser	Leu 100	Leu	Val	Pro	Thr	Ser	Gly 105	Ile	Tyr	Phe	Val	Tyr 110	Ser	Gln
Val	Val 115	Phe	Ser	Cys	Lys	Ala 120	Tyr	Ser	Pro	Lys	Ala 125	Pro	Ser	Ser	Pro
Leu 130	Tyr	Leu	Ala	His	Glu	Val 135	Cys	Leu	Phe	Ser	Ser 140	Gln	Tyr	Pro	Phe
His 145	Val	Pro	Leu	Leu	Ser 150	Ser	Gln	Lys	Met	Val 155	Tyr	Pro	Gly	Leu	Gln 160
Glu	Pro	Trp	Leu 165	His	Ser	Met	Tyr	His 170	Gly	Ala	Ala	Phe	Gln	Leu 175	Thr
Gln	Gly	Asp 180	Gln	Leu	Ser	Thr	His	Thr 185	Asp	Gly	Ile	Pro	His 190	Leu	Val
Leu	Ser 195	Pro	Ser	Thr	Val	Phe	Phe 200	Gly	Ala	Phe	Ala	Leu 205			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCGGGAT CCATGGCTAT GATGGAGGTC CAG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGCGTCTA GAGCTTAGGC AACTAAAAAG GCC

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGCGCGGAT CCATCATGGC TATGATGGAG GTCC

34

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGCGTCTA GAGCTTAGCC AACTAAAAAG GCC

33